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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=11; day=24; hr=10; min=49; sec=29; ms=158;
]
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============================================================
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************************************************************
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Reviewer Comments:

<160>   9

<170>   KopatentIn 1.71

The number provided for numeric identifier <160> must match the total
number of sequences in the file. There are 11 sequences in this sequence
listing but, 9 is given as the total in numeric identifier <160>, "<160>
9." Please make all necessary changes.

<210>   5
<211>   68
<212>   PRT
<213>   Artificial Sequence
<400>   5

For all sequences using "Artificial sequence", for numeric identifier
<213>, a mandatory feature is required to explain the source of the
genetic material. The feature consists of <220>, which remains blank,
and <223>, which states the source of the genetic material. To explain
the source, if the sequence is put together from several organisms,
please list those organisms. If the sequence is made in the laboratory,
please indicate that the sequence is synthesized. These errors appear in
other sequences in the sequence listing. Please make all necessary
changes.

★ ★

Application No: 10593413   Version No: 1.0

Input Set:

Output Set:

Started:	2008-10-28 16:16:48.335
Finished:	2008-10-28 16:16:52.980
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 645 ms
Total Warnings:	9
Total Errors:	34
No. of SeqIDs Defined:	9
Actual SeqID Count:	11

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (1)
W	213	Artificial or Unknown found in <213> in SEQ ID (2)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E	300	Invalid codon found Gly SEQID (8) POS: 337
E	300	Invalid codon found Gly SEQID (8) POS: 340
E	300	Invalid codon found Ser SEQID (8) POS: 343
E	300	Invalid codon found Ser SEQID (8) POS: 346
E	300	Invalid codon found Ser SEQID (8) POS: 349
E	300	Invalid codon found Gly SEQID (8) POS: 352
E	300	Invalid codon found Thr SEQID (8) POS: 355
E	300	Invalid codon found Val SEQID (8) POS: 358

Input Set:

Output Set:

Started:	2008-10-28 16:16:48.335
Finished:	2008-10-28 16:16:52.980
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 645 ms
Total Warnings:	9
Total Errors:	34
No. of SeqIDs Defined:	9
Actual SeqID Count:	11

Error code		Error Description
E	300	Invalid codon found Asn SEQID (8) POS: 361
E	300	Invalid codon found Pro SEQID (8) POS: 364
E	300	Invalid codon found Val SEQID (8) POS: 367
E	300	Invalid codon found Pro SEQID (8) POS: 370
E	300	Invalid codon found Thr SEQID (8) POS: 373
E	300	Invalid codon found Thr SEQID (8) POS: 376
E	300	Invalid codon found Ala SEQID (8) POS: 379
E	300	Invalid codon found Ser SEQID (8) POS: 382
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
E	323	Invalid/missing amino acid numbering SEQID (10) POS (337)
E	323	Invalid/missing amino acid numbering SEQID (10) POS (343)
E	323	Invalid/missing amino acid numbering SEQID (10) POS (352)
E	323	Invalid/missing amino acid numbering SEQID (10) POS (358)
E	323	Invalid/missing amino acid numbering SEQID (10) POS (367)
E	323	Invalid/missing amino acid numbering SEQID (10) POS (373)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)

Input Set:

Output Set:

Started:	2008-10-28 16:16:48.335
Finished:	2008-10-28 16:16:52.980
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 645 ms
Total Warnings:	9
Total Errors:	34
No. of SeqIDs Defined:	9
Actual SeqID Count:	11

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 252	Calc# of Seq. differs from actual; 9 seqIds defined; count=11

<210>   1
<211>   15
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   mimetic peptide for apolipoprotein B-100 epitope

<400>   1
Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe
 1   5   10   15

<210>   2
<211>   15
<212>   PRT
<213>   Artificial Sequence
<220>
<223>   mimetic peptide for apolipoprotein B-100 epitope

<400>   2
Arg Phe Arg Gly Leu Ile Ser Leu Ser Gln Val Tyr Leu Asp Pro
 1   5   10   15

<210>   3
<211>   15
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   mimetic peptide for apolipoprotein B-100 epitope

<400>   3
Ser Val Cys Gly Cys Pro Val Gly His His Asp Val Val Gly Leu
 1   5   10   15

<210>   4
<211>   204
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   DNA sequence for terameric mimetic peptide

<220>
<221>   CDS
<222>   (1)..(204)

<400>   4
gtc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca   48
Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala
 1   5   10   15

ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att   96
Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile
            20   25   30

gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg   144
Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
        35   40   45

att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat   192
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
    50   55   60

tgg att gca ttc   204
Trp Ile Ala Phe
 65

<210>   5
<211>   68

<212>   PRT
<213>   Artificial Sequence
<400>   5
Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala
 1   5   10   15

Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile
            20   25   30

Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
        35   40   45

Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
    50   55   60

Trp Ile Ala Phe
 65

<210>   6

<211> 180
<212> DNA
<213> Hepatitis B virus

<220>
<221> CDS
<222> (1)..(177)
<223> Hepatitis B virus preS2

<220>
<221> terminator
<222> (178)..(180)

<400> 6
atg cag tgg aac tcc acc aca ttc cac caa gct ctg cta gat ccc aga   48
Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg
 1   5   10   15

gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt tcc gga aca gta   96
Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
            20   25   30

aac cct gtt ccg act act gcc tca ccc ata tcg tca atc ttc tcg agg   144
Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
        35   40   45

act ggg gac cct gca ccg aac ctc gag cgg tca   taa   180
Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser
     50   55

<210> 7
<211> 59
<212> PRT
<213> Hepatitis B virus

<400> 7
Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg

 1   5   10   15
Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
            20   25   30

Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
        35   40   45

Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser
     50   55

<210> 8
<211> 444
<212> DNA
<213> Artificial Sequence

<220>

<223> DNA sequence for hybride polypeptide

<220>
<221> CDS
<222> (1)..(441)

<220>
<221> terminator
<222> (441)..(444)

<400> 8

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atg aga gga tcg cat cac cat cac cat cac gga tcc gat gat gat gac        48
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
1               5                   10                  15

aag atc gtc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg        96
Lys Ile Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
                20                  25                  30

att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat       144
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
        35                  40                  45

tgg att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt       192
Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val
    50                  55                  60

tat tgg att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat       240
Tyr Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp
65                  70                  75                  80

gtt tat tgg att gca ttc ctc gac atg cag tgg aac tcc acc aca ttc       288
Val Tyr Trp Ile Ala Phe Leu Asp Met Gln Trp Asn Ser Thr Thr Phe
                85                  90                  95

cac caa gct ctg cta gat ccc aga gtg agg ggc cta tat ttt cct gct       336
His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala
            100                 105                 110

ggt ggc tcc agt tcc gga aca gta aac cct gtt ccg act act gcc tca       384
Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser

        115                 120                 125

ccc ata tcg tca atc ttc tcg agg act ggg gac cct gca ccg aac ctc       432
Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Leu
    130                 135                 140

gag cgg tca taa                                                       444
Glu Arg Ser
145
```


<210> 9
<211> 147

<212> PRT
<213> Artificial Sequence

<400> 9
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
 1   5   10   15

Lys Ile Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
            20   25   30

Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
        35   40   45

Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val
      50   55   60

Tyr Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp

65   70   75   80
Val Tyr Trp Ile Ala Phe Leu Asp Met Gln Trp Asn Ser Thr Thr Phe
                85   90   95

His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala
            100   105   110

Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser
        115   120   125

Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Leu
      130   135   140

Glu Arg Ser
145

<210>   10
<211>   432
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   DNA sequence for PTB14

<220>
<221>   CDS
<222>   (1)..(429)

<400>   10
atg aga gga tcg cat cac cat cac cat cac gga tcc gat gat gat gac   48
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
 1   5   10   15

aag atc gtc gac atg cag tgg aac tcc acc aca ttc cac caa gct ctg   96
Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu

```
                20                    25                    30

cta gat ccc aga gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt        144
Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser
         35                    40                    45


tcc gga aca gta aac cct gtt ccg act act gcc tca ccc ata tcg tca        192
Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser
      50                    55                    60


atc ttc tcg aag act ggg gac cct gca ccg aac ctc gac cgt aat gtt        240
Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val
 65                    70                    75                    80


cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt aat        288
Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn
                  85                    90                    95


gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt        336
Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg
              100                   105                   110


aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac        384
Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp
115                   120                   125


cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc      t     430
Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe
     130                   135                   140


aa                                                            432



<210>   11
<211>   143
<212>   PRT
<213>   Artificial Sequence

<400>   11
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
  1               5                  10                  15


Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu
               20                  25                  30


Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser
         35                  40                  45


Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser
      50                  55                  60


Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val

 65                  70                  75                  80


Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn
```

```
              85                90                95

Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg
          100               105               110

Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp
         115               120               125

Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe
     130               135               140
```